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QY 121 HEQINGKCKMFLIEKLKIDMEKKNPSSVLREVEQCGFLHGHGDSLDLRSR 180
DB 261 HEQINGKCKMFLIEKLKIDMEKKNPSSVLREVEQCGFLHGHGDSLDLRSR 320
QY 181 RSVQGNPRA 190
DB 321 RSVQGNPRA 330

RESULT 2
Q9D4F1 PRELIMINARY; PRT; 757 AA.
ID Q9D4F1;
AC Q9D4F1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, last annotation update)
DE 4932443L08Rik protein.
GN 4932443L08Rik
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Aadachi J., Fukuda S.,
RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016573; BAB30314.1;
DR MGD: MGI:1921674; 4932443L08Rik.
SQ SEQUENCE 757 AA; 87667 MW; 320D61A71CF5DAE CRC64;

Query Match 20.5%; Score 39; DB 11; Length 757;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TFFIFLFPSPFGVCLTAITTWRLKPSADCGPFRGLP 56
DB 585 TFFIFLFPSPFGVCLTAITTWRLKPSADCGPFRGLP 623

RESULT 3
Q9UXT5 PRELIMINARY; PRT; 335 AA.
ID Q9UXT5;
AC Q9UXT5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Hypothetical protein PAB1174.
GN PAB1174.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_Taxid=29292;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248288; CAB50678.1;
DR InterPro: IPR005242; Cons_hypoth374.
DR Pfam: PF03706; UPF0104; 1.
DR TIGRFAMs: TIGR00374; TIGR00374; 1.
KM Hypothetical protein: Complete proteome.
SQ SEQUENCE 335 AA; 37288 MW; F29086681DAFCFF CRC64;

Query Match 4.2%; Score 8; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 ILTLIVLI 101
DB 158 ILTLIVLI 165

RESULT 4
Q9XUX9 PRELIMINARY; PRT; 351 AA.
ID Q9XUX9;
AC Q9XUX9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE F57G4.4 protein.
GN F57G4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Ainscough R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
RC MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z81554; CAB04503.1;
DR InterPro: IPR002900; DUF38.
DR InterPro: IPR001810; F-box.
DR Pfam: PF01827; DUF38; 1.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
DR PROSITE: PSS0181; FBOX; 1.
SQ SEQUENCE 351 AA; 40374 MW; 97F396F5BF82CA31 CRC64;

Query Match 4.2%; Score 8; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DGSIDLRS 179
DB 55 DGSIDLRS 62

RESULT 5
Q97KL3 PRELIMINARY; PRT; 752 AA.
ID Q97KL3;
AC Q97KL3;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, last annotation update)
DE ATPase with chaperon activity, two ATP-binding domains, ClpC
DE orthologs.

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GN CAC0904.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
 Ratatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL, AE007605; AK78880.1; -.
 DR InterPro: IPR003593; AAA_Arpase.
 DR InterPro: IPR003599; AAA_Arpase_cent.
 DR InterPro: IPR001270; Chaprinin_c1pa/B.
 DR Pfam: PF00004; AAA; 2.
 DR PRINTS: PR00300; CLPPROTEASEA.
 DR SMART: SM00382; AAA; 2.
 DR PROSITE: PS00871; CLPA_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 752 AA; 84925 MW; 57B4C4B6C47D80A6 CRC64;

Query Match 4.2%; Score 8; DB 16; Length 752;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 IINEGDK 131
 |||||
 DB 678 IINEGDK 685

RESULT 6
 ID 095KK4 PRELIMINARY; PRT; 148 AA.
 AC 095KK4.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Single-stranded DNA binding precursor.
 GN SSB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duresne C., Gueride M.;
 RT "Identification and expression of cDNA and pseudogene coding for the
 rabbit mitochondrial single-strand DNA-binding protein.";
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ311162; CAC38115.1; -.
 DR InterPro: IPR000424; SSB_protein.
 DR Pfam: PF00436; SSB; 1.
 DR TIGRfams: TIGR00621; ssb; 1.
 DR PROSITE: PS00735; SSB_1; UNKNOWN_1.
 DR PROSITE: PS00736; SSB_2; UNKNOWN_1.
 KW SIGNAL.
 FT CHAIN 1 16 POTENTIAL.
 FT SIGNAL 17 148 POTENTIAL.
 SQ SEQUENCE 148 AA; 17155 MW; 9AF894B6468C6C43 CRC64;

Query Match 3.7%; Score 7; DB 6; Length 148;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLVR 157
 |||||
 DB 22 SSVLVR 28

RESULT 7
 ID 08R2K3 PRELIMINARY; PRT; 148 AA.
 AC 08R2K3.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Similar to single-stranded DNA binding protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY GLAND;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC028648; AAH28648.1; -.
 SQ SEQUENCE 148 AA; 17157 MW; ESC00016DF6B84CD CRC64;

Query Match 3.7%; Score 7; DB 11; Length 148;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLVR 157
 |||||
 DB 22 SSVLVR 28

RESULT 8
 ID 09CYR0 PRELIMINARY; PRT; 152 AA.
 AC 09CYR0.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 2810480P10R1k protein.
 GN 2810480P10R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana T.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Glass C., King B., Kochiya H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK013425; BAB28650.1; -.
 DR HSSP: Q04837; 3UTL.
 DR MGD: MG1:1920040; 2810480P10R1K.
 DR InterPro: IPR000424; SSB_protein.
 DR Pfam: PF00436; SSB; 1.

DR TIGRFAMs; TIGR00621; ssb; 1.
 DR PROSITE; PS00735; SSB_1; 1.
 DR PROSITE; PS00736; SSB_2; 1.
 SQ SEQUENCE 152 AA; 17319 MW; 719B9F03C4C0D1EE CRC64;

Query Match 3.7%; Score 7; DB 11; Length 152;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLER 157
 |||||
 Db 22 SSVLER 28

RESULT 9

ID 016583 PRELIMINARY; PRT; 170 AA.

AC 016583; 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

GN C33C12.2. Hypothetical 19.8 kda protein.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA MEDLINE=99069613; PubMed=9851916;

RT None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium."

RT Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Gattung S., Scheet P.;

RT "The sequence of C. elegans cosmid C33C12.2";

RT Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.;"

RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

KW EMBL; AF016662; AAB66062.1; -.

SQ SEQUENCE 170 AA; 19762 MW; D6C3E6F4BEDE52D0 CRC64;

Query Match 3.7%; Score 7; DB 5; Length 170;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 FLIEKL 139
 |||||
 Db 56 FLIEKL 62

RESULT 10

ID 0980A6 PRELIMINARY; PRT; 180 AA.

AC 0980A6; 01-OCT-2001 (TREMBLrel. 18, Created)

DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)

GN MYPU_4600. Hypothetical protein MYPU_4600.

OS Mycoplasma pulmonis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

OC Mycoplasmataceae; Mycoplasma.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chandraud I., Hellig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dydyg K., Wroblewski H., Viart A., Rocha E.P.C.,
 RA Blanchard A.;

RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis.;"

RL Nucleic Acids Res. 29:2145-2153(2001).

DR EMBL; AF445564; CAC13633.1; -.

DR Mypulist; MYPU_4600; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 180 AA; 20466 MW; 6BA8C675358D167B CRC64;

Query Match 3.7%; Score 7; DB 16; Length 180;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 135 IEKLKL 141
 |||||
 Db 142 IEKLKL 148

RESULT 11

ID 092DQ9 PRELIMINARY; PRT; 202 AA.

AC 092DQ9; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN LIN0754. Hypothetical protein lin0754.

OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Listeriaceae; Listeria.

OX NCBI_TaxID=1642;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CLIP 11262 / SEROVAR 6A;

RA PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Ertian K.-D., Esli H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,

RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

RT "Comparative genomics of Listeria species.;"

RL Science 294:849-852(2001).

Query Match 3.7%; Score 7; DB 16; Length 202;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 171 HDGSLDL 177
 |||||
 Db 62 HDGSLDL 68

RESULT 12

ID 08Y8Y2 PRELIMINARY; PRT; 202 AA.

AC 08Y8Y2; 08Y8Y2;

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein Imo0760.
 GN Imo0760.
 OS *Listeria monocytogenes*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 CX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-E / SEROVAR 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
 RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouni F., Couve E., de Daruvar A., Denoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schuener T., Simoes N., Trieretz A.,
 RA Vaquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RL Science 294:849-852(2001).
 DR EMBL: AL591976; CAC98838.1; -
 DR Lifestlist: IM000760; -
 DR Interpro: IPR000379; Ser_estrs_site.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 202 AA; 22264 MW; 37CE2E2A8872E347 CRC64;

Query Match 3.7%; Score 7; DB 16; Length 202;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 HDGSIDL 177
 |||||
 DB 62 HDGSIDL 68

RESULT 13
 Q48599 PRELIMINARY; PRT; 214 AA.
 AC 048599;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NISG.
 GN NISG.
 OS *Lactococcus lactis*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 CX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6r3;
 RX MEDLINE=95314241; PubMed=7793910;
 RA Slegers K., Entian K.D.;
 RT "Genes involved in immunity to the lantibiotic nisin in *Lactococcus*
 RT *lactis* 6r3.";
 RL Appl. Environ. Microbiol. 61:1082-1089(1995).
 DR EMBL: U17255; AAC43329.1; -
 SQ SEQUENCE 214 AA; 24193 MW; 1648256FC07C9A85 CRC64;

Query Match 3.7%; Score 7; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 FILFFPS 28
 |||||
 DB 96 FILFFPS 102

RESULT 14
 Q48637 PRELIMINARY; PRT; 214 AA.
 AC 048637;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Membrane protein.
 GN NISG.
 OS *Lactococcus lactis*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 CX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452385; PubMed=10524754;
 RA Immonen T., Saris P.E.J.;
 RT "Characterization of the nifFG operon of the nisin Z producing
 RT *Lactococcus lactis* subsp. *lactis* N8 strain.";
 RL DNA Seq. 9:263-274(1998).
 DR EMBL: Z29363; CAA82549.1; -
 SQ SEQUENCE 214 AA; 24174 MW; 8C28257F1A10B2F9 CRC64;

Query Match 3.7%; Score 7; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 FILFFPS 28
 |||||
 DB 96 FILFFPS 102

RESULT 15
 Q96XL5 PRELIMINARY; PRT; 231 AA.
 AC 096XL5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical protein ST2501.
 GN ST2501.
 OS *Sulfolobus tokodaii*.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 CX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT *Crenarchaeon*, *Sulfolobus tokodaii* strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000990; BAB67612.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 231 AA; 26846 MW; F59852E1099E7CD1 CRC64;

Query Match 3.7%; Score 7; DB 17; Length 231;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 IINEGND 130
 |||||
 DB 223 IINEGND 229

RESULT 16

OS0296
ID 050296 PRELIMINARY; PRT; 244 AA.
AC 050296;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP-binding subunit.
GN DEVA.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29413;
RX MEDLINE=98440130; PubMed=9767151;
RA Fiedler G., Arnold M., Maldener I.;
RT "Sequence and mutational analysis of the devCA gene cluster encoding a putative ABC transporter in the cyanobacterium Anabaena variabilis
RT ATCC 29413.";
RL Blochl M. Biophys. Acta 1375:140-143(1998).
CC EMBL; AUT003195; CA05977.1; -;
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KM ATP-binding; Transport.
SQ SEQUENCE 244 AA; 26709 MW; 785452AE915B6D20 CRC64;

Query Match 3.7%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RSV0EGN 187
Db 60 RSV0EGN 66
|||||

RESULT 17
057281 PRELIMINARY; PRT; 244 AA.
ID 057281;
AC 057281;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE PCC7120 DEVA. DEVA genes, ORF2 & ORF3 (Heterocyst specific
DE ABC-transporter, ATP-binding subunit).
GN DEVA OR ALR3712.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC7120;
RX Fiedler G., Arnold M., Maldener I.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PASTEUR C NO. 7120;
RX MEDLINE=95095923; PubMed=8002578;
RA Maldener I., Fiedler G., Ernst A., Fernandez-Pinas F., Molk C.P.;
RT "Characterization of devA, a gene required for the maturation of
RT proheterocysts in the cyanobacterium Anabaena sp. strain PCC 7120."
RL Bacteriol. 176:7543-7549(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iritaguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; X99672; CA67987.1; -;
DR EMBL; X75422; CA53174.1; -;
DR EMBL; AP003594; BAB75411.1; -;
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KM ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 244 AA; 26723 MW; 34182185A5C0A4B CRC64;

Query Match 3.7%; Score 7; DB 16; Length 244;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RSV0EGN 187
Db 60 RSV0EGN 66
|||||

RESULT 18
098R89 PRELIMINARY; PRT; 245 AA.
ID 098R89;
AC 098R89;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Hypothetical protein MYPU_1210.
GN MYPU_1210.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Vlati A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445563; CAC13294.1; -;
DR MYPULIST; MYPU_1210; -;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 245 AA; 28756 MW; 54DAE7AFCF21B29 CRC64;

Query Match 3.7%; Score 7; DB 16; Length 245;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 TLIVLII 102
Db 223 TLIVLII 229
|||||

RESULT 19
047800 PRELIMINARY; PRT; 251 AA.
ID 047800;
AC 047800;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
GN CTB.
OS Gymnodraco acuticeps (Antarctic dragonfish).

OG Mitochondrion.
 OC Euryarchaeota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes;
 OC Notothenioidae; Bathyrdaconidae; Gymnodraco.
 OX NCBI_TaxID=8218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Chen W.J., Bonillo C., Lecointre G.;
 RT "Phylogeny of the Channichthyidae (Notothenioidae, Teleostei) based on
 two mitochondrial genes.";
 RL (In) di Prisco G., Pisano E., Clarke A. (eds.);
 RL FISHES OF ANTARCTICA. A BIOLOGICAL OVERVIEW, pp.1-1,
 RL Springer-Verlag Publishers (1998).
 CC -1- FUNCTION: COMPONENT OF THE UBQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL; AF037109; AAC04790.1; -
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF00033; cytochrome_b_c1.
 DR PROSITE: PS00193; CYTOCHROME_B_Q0; UNKNOWN_1.
 KW Election transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 251 251
 SQ SEQUENCE 251 AA; 27682 MW; A9B97A9B9484B11 CRC64;
 Query Match 3.7%; Score 7; DB 8; Length 251;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21 IFLFFP 27
 Db 235 IFLFFP 241

RESULT 20
 ID 065045 PRELIMINARY; PRT; 282 AA.
 AC 065045;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Probable aquaporin.
 GN SB01.
 OS Picea mariana (Black spruce).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 OX NCBI_TaxID=3335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278823; PubMed=9611216;
 RA Perry D.J., Bousquet J.;
 RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,
 RT characterization and analysis of linkage in black spruce.";
 RL Genetics 149:1089-1098(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
 DR EMBL; AF051202; AAC32107.1; -
 DR HSSP: P29972; IFOY.
 DR InterPro: IPR000425; MIP_family.
 DR Pfam: PF00230; MIP; 1.
 DR PRINTS: PR00783; MIMTRINSCP.
 DR ProDom: PD000295; MIP_family; 1.
 DR TIGRfams: TIGR00861; MIP; 1.

DR PROSITE: PS00221; MIP; 1.
 KW Porin; Transmembrane; Transport.
 KW SEQUENCE 282 AA; 30154 MW; 89204AACAA9DB340 CRC64;
 Query Match 3.7%; Score 7; DB 10; Length 282;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 159 EVEQGF 165
 Db 8 EVEQGF 14

RESULT 21
 ID 08RS30 PRELIMINARY; PRT; 298 AA.
 AC 08RS30;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ORE5.
 GN ORE5.
 OS Comamonas acidovorans (Pseudomonas acidovorans).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Delftia.
 OX NCBI_TaxID=80866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B;
 RC Sota M., Endo M., Nitta K., Kawasaki H., Tsuda M.;
 RT "Characterization of a class II defective transposon carrying two
 RT haloacetate dehalogenase genes from Delftia acidovorans plasmid
 RT PU0H1.";
 RL Appl. Environ. Microbiol. 0:0-0(2002).
 DR EMBL; AB049198; BAB8587.1; -
 KW Plasmid.
 SQ SEQUENCE 298 AA; 32798 MW; 8FC1102E7A7EPE17 CRC64;
 Query Match 3.7%; Score 7; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 178 RSRRSVQ 184
 Db 52 RSRRSVQ 58

RESULT 22
 ID 029940 PRELIMINARY; PRT; 324 AA.
 AC 029940;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE UDP-glucose dehydrogenase (UGD-1).
 GN AF0302.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kervatage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischman R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Welch C.I., McNeill L.K., Badger J.H., Glodok A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

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RA  Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA  Venter J.C.;
RT  "The complete genome sequence of the hyperthermophilic, sulphate-
RT  reducing archaeon Archaeoglobus fulgidus.";
RL  Nature 390:364-370(1997).
DR  EMBL: AE001084; MAB90929.1; -.
DR  TIGR: AF0302; -.
DR  InterPro: IPR001732; UDPG_MGDP_dh.
DR  Pfam: PF00984; UDPG_MGDP_dh_N: 1.
DR  Pfam: PF03721; UDPG_MGDP_dh_N: 1.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 324 AA; 35838 MW; 36D058B8C00B08 CRC64;

Query Match 3.7%; Score 7; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DGSIDL 178
DB 89 DGSIDL 95

RESULT 23
ID 093259 PRELIMINARY; PRT; 325 AA.
AC 093259;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Melanocortin 3-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RC MEDLINE=9914114; PubMed=9990303;
RA Takeuchi S., Takahashi S.;
RT "A possible involvement of melanocortin 3-receptor in the regulation
RT of adrenal gland function in the chicken.";
RL Blochm. Biophys. Acta 1448:512-518(1998).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AB017137; BAA32555.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_P1_1.1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_P1_2.1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 325 AA; 36601 MW; 94FA6631ED144C17 CRC64;

Query Match 3.7%; Score 7; DB 13; Length 325;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LTLIVL 101
DB 162 LTLIVL 168

RESULT 24
ID 09XXA9 PRELIMINARY; PRT; 327 AA.
AC 09XXA9;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Y94A7B.5 protein.
DE Y94A7B.5.
GN Y94A7B.5
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

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OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=99069613; PubMed=9851916;
RA none;
RT "genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: AL023856; CAI19567.1; -.
DR InterPro: IPR003003; 7TM_chemo2.
DR InterPro: IPR000168; 7TM_nematode.
DR Pfam: PF01604; 7tm_5.1.
SQ SEQUENCE 327 AA; 37108 MW; B251B168C77BBBD CRC64;

Query Match 3.7%; Score 7; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LTLIVL 101
DB 197 LTLIVL 203

RESULT 25
ID 051564 PRELIMINARY; PRT; 330 AA.
AC 051564;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein BB0619.
GN BB0619.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RC MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kierlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL: AE001163; AAC6977.1; -.
DR TIGR: BB0619; -.
DR InterPro: IPR003156; DHHA1.
DR InterPro: IPR001667; Ppesterase.
DR Pfam: PF01368; DHHA1.1.
DR Pfam: PF02272; DHHA1.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 330 AA; 37377 MW; 392DB8DF6160DEA6 CRC64;

Query Match 3.7%; Score 7; DB 16; Length 330;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 FLIEKLI 139
DB 139 FLIEKLI 145

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RESULT 26
O9RLV9 PRELIMINARY: PRT: 335 AA.
ID 09RLV9:
AC 09RLV9:
DT 01-MAR-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sphingomyelinase-c.
OS Listeria ivanovi.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1638;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19119;
RX MEDLINE-99348382; PubMed-10417642;
RA Gonzalez-Zorn B., Dominguez-Bernal G., Suarez M., Ripio M.T., Vega Y.,
RA Novella S., Vazquez-Boland J.A.;
RT "The smcl gene of Listeria ivanovi encodes a sphingomyelinase C that
RT mediates bacterial escape from the phagocytic vacuole.";
RL Mol. Microbiol. 33:510-523(1999).
DR EMBL, Y09477; CAI70683.2; -.
DR InterPro: IPR005135; Exo_endo_phos.
DR Pfam: PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 335 AA; 38455 MW; 46F39858A8434D7 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 17 FIFLFF 23

RESULT 27
O8XDV8 PRELIMINARY: PRT: 338 AA.
ID O8XDV8:
AC O8XDV8:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Periplasmic binding protein component of Pn transporter.
GN PHND OR 25707 OR ECS5087.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoculis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE-21156331; PubMed-1128796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kudara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL, AE005643; AAC59304.1; -.
DR EMBL, AP002568; BAB38510.1; -.

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KW Complete proteome.
SQ SEQUENCE 338 AA; 37418 MW; A6AFC8CFFAC9D6B5 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LODMEK 147
DB 54 LODMEK 60

RESULT 28
O30478 PRELIMINARY: PRT: 340 AA.
ID O30478:
AC O30478:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative pteridine-dependent dioxigenase.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29253;
RX MEDLINE-98085969; PubMed-9426000;
RA Ruan X., Stassi D., Lax S.A., Katz L.;
RT "A second type-I PKS gene cluster isolated from Streptomyces
RT hygroscopicus ATCC 29253, a rapamycin-producing strain.";
RL Gene 203:1-9(1997).
DR EMBL, AF007101; AAC38060.1; -.
DR InterPro: IPR00543; Yj9F-like.
DR Pfam: PF01042; DPF0076; 1.
SQ SEQUENCE 340 AA; 37429 MW; 74B9440290366D8B CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 NPSSLVL 155
DB 2 NPSSLVL 8

RESULT 29
O98KF2 PRELIMINARY: PRT: 344 AA.
ID O98KF2:
AC O98KF2:
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Penicillin protein of ribose ABC transporter.
GN MEL1505.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF303099;
RX MEDLINE-21082930; PubMed-11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL, AP002997; BAB48862.1; -.

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DR InterPro: IPR001851; Bac_inmem_transp.
DR InterPro: IPR001064; Crystallin.
DR Pfam: PF02653; BPD_transp_2; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 344 AA; 36981 MW; AE49A22DD070150 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 QIINEGK 129
Db 162 QIINEGK 168

RESULT 30
Q8RFH8 PRELIMINARY; PRT; 350 AA.
AC Q8RFH8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical cytosolic protein FN0719.
GN FN0719.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
ON NCBI_TaxID=76856;
RX MEDLINE=1889109; PubMed=1889109;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Lonslein M., Kyrides N., Overbeek R.,
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RL nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL: AE010582; AAL94915.1; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 350 AA; 41804 MW; 21A901CF46CD50D8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LIEKLK 140
Db 335 LIEKLK 341

RESULT 31
Q9MKL8 PRELIMINARY; PRT; 354 AA.
AC Q9MKL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus abbreviatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
ON NCBI_TaxID=114446;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F.;
RA Prueser F., Brueckner M., Mossakowski D.;
RA "Colonization of Canary Islands by Carabus species: evidence from

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RT different character complexes."
RL (In) Brandmayr P., Lovel G., Brandmayr T.Z., Casale A.,
RL Vigna Taglianti A. (eds.);
RL Natural history and applied ecology of carabid beetles (Proceedings of
RL the 9th European carabidologist meeting), pp.1-1, Pensoft,
RL Sofia (2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AF231695; AAF61942.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 354 AA; 40667 MW; B0AE2E15FE5396C2 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 32
Q9MEG7 PRELIMINARY; PRT; 355 AA.
AC Q9MEG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
ON NCBI_TaxID=118064;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomimaga O., Saito S., Kim C.G., Otsawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RL from mitochondrial ND5 gene sequences."
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB039808; BAA92457.1; -.
DR EMBL: AB039804; BAA92453.1; -.
DR EMBL: AB039805; BAA92454.1; -.
DR EMBL: AB039806; BAA92455.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40947 MW; 0556E113E1D97D80 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 33
Q9MEG6 PRELIMINARY; PRT; 355 AA.
AC Q9MEG6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).

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GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomlinaga O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RT from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB039809; BAA92458.1; -.
DR EMBL; AB039807; BAA92456.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER
SQ SEQUENCE 355 AA; 40961 MW; 0556E113FF289280 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 34
Q9MEC7 PRELIMINARY; PRT; 355 AA.
AC Q9MEC7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus granulatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-55; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomlinaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OH33;
RA Sota T., Vogler A.P.;
RT "Incongruence of mitochondrial and nuclear gene trees in the carabid
RT beetles Ohomopterus.";
RL Syst. Biol. 0:0-0(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041069; BAA94628.1; -.
DR EMBL; AF219473; AAF62460.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER
SQ SEQUENCE 355 AA; 40873 MW; 1AFA4B4EA9BA16BA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 35
Q9ME44 PRELIMINARY; PRT; 355 AA.
AC Q9ME44;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus aeneus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=49192;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-35, 31, 33, 36, AND 34; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomlinaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041059; BAA94618.1; -.
DR EMBL; AB041054; BAA94613.1; -.
DR EMBL; AB041056; BAA94615.1; -.
DR EMBL; AB041057; BAA94616.1; -.
DR EMBL; AB041058; BAA94617.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER
SQ SEQUENCE 355 AA; 40824 MW; 5401A867989B3D75 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 36
Q9ME14 PRELIMINARY; PRT; 355 AA.
AC Q9ME14;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis porrecticollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87295;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-37, 33, 34, AND 36; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomlinaga O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands inferred from
RT Mitochondrial ND5 Gene Sequences.";

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RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB022590; BAA74502.1; -;
DR EMBL: AB022586; BAA74498.1; -;
DR EMBL: AB022587; BAA74499.1; -;
DR EMBL: AB022589; BAA74501.1; -;
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40914 MW; 67A294D3AE3C4B30 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 37
Q9MD25 PRELIMINARY; PRT; 355 AA.
AC 09MD25;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOKKAIDO-NIIKAPPUB, AND HOKKAIDO-SAROMA3; TISSUE=THORAX MUSCLE;
RA Su Z. H., Tomlinaga O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RT from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB039800; BAA92449.1; -;
DR EMBL: AB039796; BAA92445.1; -;
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40899 MW; 704B4C5FBCA13D00 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 38
Q9MDT2 PRELIMINARY; PRT; 355 AA.
AC 09MDT2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis kansaiensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23, AND 22; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomlinaga O., Su Z.H., Okamoto M., Imura Y., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands inferred from
RT Mitochondrial ND5 gene sequences.";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB022576; BAA74488.1; -;
DR EMBL: AB022575; BAA74487.1; -;
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40944 MW; 8A2E3165B68D5F10 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 39
Q9MDT0 PRELIMINARY; PRT; 355 AA.
AC 09MDT0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus granulatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=45, 43, AND 39; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomlinaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB041073; BAA94632.1; -;
DR EMBL: AB041070; BAA94629.1; -;
DR EMBL: AB041071; BAA94630.1; -;
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40803 MW; 8BC0FE5FEB605A0 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 40
Q9MDS6

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ID 09MDS6 PRELIMINARY; PRT; 355 AA.
AC 09MDS6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN NDS.
OS Carabus porrecticollis kansaiensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OC NCBI_TaxID=87296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomioka O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands Inferred from
RT Mitochondrial ND5 Gene Sequences.";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB022585; BAA74487.1; -
DR EMBL; AB022571; BAA74483.1; -
DR EMBL; AB022573; BAA74485.1; -
DR EMBL; AB022574; BAA74486.1; -
DR EMBL; AB022577; BAA74489.1; -
DR EMBL; AB022578; BAA74490.1; -
DR EMBL; AB022579; BAA74491.1; -
DR EMBL; AB022580; BAA74492.1; -
DR EMBL; AB022581; BAA74493.1; -
DR EMBL; AB022582; BAA74494.1; -
DR EMBL; AB022583; BAA74495.1; -
DR EMBL; AB022584; BAA74496.1; -
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40914 MW; 8D54BDA4BAF52A11 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 41
O9MDR6 PRELIMINARY; PRT; 355 AA.
AC 09MDR6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN NDS.
OS Carabus granulatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OC NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=49, AND 47; TISSUE=THORAX MUSCLE;
RA MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna Inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

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DR EMBL; AB041067; BAA94626.1; -
DR EMBL; AB041066; BAA94625.1; -
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1.1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40860 MW; 927E920321AE5665 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 42
O9MDR4 PRELIMINARY; PRT; 355 AA.
AC 09MDR4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN NDS.
OS Carabus munakatai.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OC NCBI_TaxID=120937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THORAX MUSCLE;
RA MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna Inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041084; BAA94643.1; -
DR EMBL; AB041083; BAA94642.1; -
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1.1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40895 MW; 956C1181F08A06FE CRC64;

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 43
O9MDR3 PRELIMINARY; PRT; 355 AA.
AC 09MDR3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN NDS.
OS Carabus schrenckii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OC NCBI_TaxID=120935;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z. H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB041081; BAA94640.1; -.
DR EMBL: AB041080; BAA94639.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40868 MW; 977A20EC3532FD9C CRC64;

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Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 20 FIFLFF 26
Db 157 FIFLFF 163

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RESULT 44
ID 09MD3 PRELIMINARY; PRT; 355 AA.
AC 09MD3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis porrecticollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87295;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12, 1, 2, 3, 4, 5, 6, 9, 10, AND 11; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomioka O., Su Z. H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
(Coleoptera, Carabidae) in the Japanese Islands inferred from
mitochondrial ND5 Gene Sequences";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB022565; BAA74477.1; -.
DR EMBL: AB022555; BAA74467.1; -.
DR EMBL: AB022556; BAA74468.1; -.
DR EMBL: AB022557; BAA74469.1; -.
DR EMBL: AB022558; BAA74470.1; -.
DR EMBL: AB022559; BAA74471.1; -.
DR EMBL: AB022560; BAA74472.1; -.
DR EMBL: AB022562; BAA74474.1; -.
DR EMBL: AB022563; BAA74475.1; -.
DR EMBL: AB022564; BAA74476.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40916 MW; E6B39DF6723A8FEB CRC64;

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Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 20 FIFLFF 26
Db 157 FIFLFF 163

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RESULT 45
ID 09MD3 PRELIMINARY; PRT; 355 AA.
AC 09MD3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOKKAIDO-KOSHIRO2, AND HOKKAIDO-NEWMURO1; TISSUE=THORAX MUSCLE;
RA Su Z. H., Tomioka O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB039795; BAA92444.1; -.
DR EMBL: AB039794; BAA92443.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40959 MW; F071F1D770E4FBD4 CRC64;

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Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 20 FIFLFF 26
Db 157 FIFLFF 163

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Search completed: November 9, 2002, 07:30:24
Job time : 95 secs

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